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Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2007; month=11; day=28; hr=18; min=49; sec=34; ms=540;
]

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Application No: 09776874 Version No: 3.1

Input Set:

Output Set:

Started: 2007-11-28 18:48:15.849
Finished: 2007-11-28 18:48:19.043
Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 194 ms
Total Warnings: 32
Total Errors: 3
No. of SeqIDs Defined: 47
Actual SeqID Count: 47

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
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W 213	Artificial or Unknown found in <213> in SEQ ID (7)
E 201	Mandatory field data missing in <223> in SEQ ID (11)
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W 213	Artificial or Unknown found in <213> in SEQ ID (17)
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W 213	Artificial or Unknown found in <213> in SEQ ID (23)
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W 213	Artificial or Unknown found in <213> in SEQ ID (25)
W 213	Artificial or Unknown found in <213> in SEQ ID (26)
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Input Set:

Output Set:

Started: 2007-11-28 18:48:15.849
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Total Warnings: 32
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No. of SeqIDs Defined: 47
Actual SeqID Count: 47

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (28)
W 213	Artificial or Unknown found in <213> in SEQ ID (29) This error has occurred more than 20 times, will not be displayed
E 201	Mandatory field data missing in <223> in SEQ ID (45)

SEQUENCE LISTING

<110> Pecker, Iris
Vlodavsky , Israel
Feinstein, Elena

<120> POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY
AND EXPRESSION OF SAME IN GENETICALLY MODIFIED CELLS

<130> 01/22603

<140> 09776874
<141> 2001-02-06

<150> US 08/922,170

<151> 1997-09-02

<150> US 09/109,386

<151> 1998-07-10

<150> PCT/US98/17954

<151> 1998-08-31

<160> 47

<170> PatentIn version 3.1

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<210> 9

<211> 1721

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tcaagaacag cacctactca agaagctctg tagatgtgct atacactttt gcaaactgct 600

caggacttggaa cttgatcttt ggccctaaatg cggttattaag aacagcagat ttgcagtgaa 660

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<213> Homo sapiens

<400> 10

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35 40 45

Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala Asn
50 55 60

Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys Leu
65 70 75 80

Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly
85 90 95

Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr Phe
100 105 110

Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys Lys
115 120 125

Tyr Gly Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu Trp
130 135 140

Pro Tyr Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys Phe
145 150 155 160

Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr Phe
165 170 175

Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu Leu
180 185 190

Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu Leu
195 200 205

Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly Asn
210 215 220

Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly Ser
225 230 235 240

Gln Leu Gly Glu Asp Tyr Ile Gln Leu His Lys Leu Leu Arg Lys Ser
245 250 255

Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro Arg
260 265 270

Arg Lys Thr Ala Lys Met Leu Lys Ser Phe Leu Lys Ala Gly Gly Glu
275 280 285

Val Ile Asp Ser Val Thr Trp His His Tyr Tyr Leu Asn Gly Arg Thr
290 295 300

Ala Thr Arg Glu Asp Phe Leu Asn Pro Asp Val Leu Asp Ile Phe Ile
305 310 315 320

Ser Ser Val Gln Lys Val Phe Gln Val Val Glu Ser Thr Arg Pro Gly
325 330 335

Lys Lys Val Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly Gly Ala
340 345 350

Pro Leu Leu Ser Asp Thr Phe Ala Ala Gly Phe Met Trp Leu Asp Lys

355

360

365

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370 375 380

Phe Phe Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe Asp Pro
385 390 395 400

Leu Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu Val Gly Thr
405 410 415

Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu Arg
420 425 430

Val Tyr Leu His Cys Thr Asn Thr Asp Asn Pro Arg Tyr Lys Glu Gly
435 440 445

Asp Leu Thr Leu Tyr Ala Ile Asn Leu His Asn Val Thr Lys Tyr Leu
450 455 460

Arg Leu Pro Tyr Pro Phe Ser Asn Lys Gln Val Asp Lys Tyr Leu Leu
465 470 475 480

Arg Pro Leu Gly Pro His Gly Leu Leu Ser Lys Ser Val Gln Leu Asn
485 490 495

Gly Leu Thr Leu Lys Met Val Asp Asp Gln Thr Leu Pro Pro Leu Met
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Glu Lys Pro Leu Arg Pro Gly Ser Ser Leu Gly Leu Pro Ala Phe Ser
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<213> Homo sapiens

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1	5		10		15			
ctg ctc	ctg ggg	ccg ctg	ggt ccc	ctc tcc	cct ggc	gcc ctg	ccc cga	155
Leu Leu	Leu Gly	Pro Leu	Gly Pro	Leu Ser	Pro Gly	Ala Leu	Pro Arg	
20	25			30				
cct gcg	caa gca	cag gac	gtc gtg	gac ctg	gac ttc	ttc acc	cag gag	203
Pro Ala	Gln Ala	Gln Asp	Val Val	Asp Leu	Asp Phe	Phe Thr	Gln Glu	
35	40			45				
ccg ctg	cac ctg	gtg agc	ccc tcg	ttc ctg	tcc gtc	acc att	gac gcc	251
Pro Leu	His Leu	Val Ser	Pro Ser	Phe Leu	Ser Val	Thr Ile	Asp Ala	
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aac ctg	gcc acg	gac ccg	cggttcc	atc ctc	ctg ggt	tct cca	aag	299
Asn Leu	Ala Thr	Asp Pro	Arg Phe	Ieu Ile	Leu Leu	Gly Ser	Pro Lys	
65	70			75				
ctt cgt	acc ttg	gcc aga	ggcttg	tct cct	gcgtac	ctg agg	ttt ggt	347
Leu Arg	Thr Leu	Ala Arg	Gly Leu	Ser Pro	Ala Tyr	Leu Arg	Phe Gly	
80	85			90		95		
ggc acc	aag aca	gac ttc	cta att	ttc gat	ccc aag	aag gaa	tca acc	395
Gly Thr	Lys Thr	Asp Phe	Leu Ile	Phe Asp	Pro Lys	Lys Glu	Ser Thr	
100	105			110				
ttt gaa	gag aga	agt tac	tgg caa	tct caa	gtc aac	cag gat	att tgc	443
Phe Glu	Glu Arg	Ser Tyr	Trp Gln	Ser Gln	Val Asn	Gln Asp	Ile Cys	
115	120			125				
aaa tat	gga tcc	atc cct	cct gat	gtg gag	gag aag	tta cgg	ttg gaa	491
Lys Tyr	Gly Ser	Ile Pro	Pro Asp	Val Glu	Glu Lys	Lys Leu	Arg Leu	
130	135			140				
tgg ccc	tac cag	gag caa	ttg cta	ctc cga	gaa cac	tac cag	aaa aag	539
Trp Pro	Tyr Gln	Glu Gln	Leu Leu	Leu Arg	Glu His	Tyr Gln	Lys Lys	
145	150			155				
ttc aag	aac acc	acc tac	tca aga	agc tct	gta gat	gtg cta	tac act	587
Phe Lys	Asn Ser	Thr Tyr	Ser Arg	Ser Ser	Val Asp	Val Leu	Tyr Thr	
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Phe Ala	Asn Cys	Ser Gly	Leu Asp	Ile Phe	Gly Leu	Asn Ala	Leu	
180	185			190				
tta aga	aca gca	gat ttg	cag tgg	aac agt	tct aat	gct cag	ttg ctc	683
Leu Arg	Thr Ala	Asp Leu	Gln Trp	Asn Ser	Ser Asn	Ala Gln	Leu Leu	
195	200			205				
ctg gac	tac tgc	tct tcc	aag ggg	tat aac	att tct	tgg gaa	cta ggc	731

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Asn	Glu	Pro	Asn	Ser	Phe	Leu	Lys	Lys	Ala	Asp	Ile	Phe	Ile	Asn	Gly	
225							230					235				
tgc	cag	tta	gga	gaa	gat	tat	att	caa	ttg	cat	aaa	ctt	cta	aga	aag	827
Ser	Gln	Leu	Gly	Glu	Asp	Tyr	Ile	Gln	Leu	His	Lys	Leu	Leu	Arg	Lys	
240							245					250				255
tcc	acc	ttc	aaa	aat	gca	aaa	ctc	tat	ggt	cct	gat	gtt	ggt	cag	cct	875
Ser	Thr	Phe	Lys	Asn	Ala	Lys	Leu	Tyr	Gly	Pro	Asp	Val	Gly	Gln	Pro	
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cga	aga	aag	acg	gct	aag	atg	ctg	aag	agc	ttc	ctg	aag	gct	ggt	gga	923
Arg	Arg	Lys	Thr	Ala	Lys	Met	Leu	Lys	Ser	Phe	Leu	Lys	Ala	Gly	Gly	
275							280					285				
gaa	gtg	att	gat	tca	gtt	aca	tgg	cat	cac	tac	tat	ttg	aat	gga	cgg	971
Glu	Val	Ile	Asp	Ser	Val	Thr	Trp	His	His	Tyr	Tyr	Leu	Asn	Gly	Arg	
290							295					300				
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Thr	Ala	Thr	Arg	Glu	Asp	Phe	Leu	Asn	Pro	Asp	Val	Leu	Asp	Ile	Phe	
305							310					315				
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Ile	Ser	Ser	Val	Gln	Lys	Val	Phe	Gln	Val	Val	Glu	Ser	Thr	Arg	Pro	
320							325					330				335
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Gly	Lys	Lys	Val	Trp	Leu	Gly	Glu	Thr	Ser	Ser	Ala	Tyr	Gly	Gly		
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Ala	Pro	Leu	Leu	Ser	Asp	Thr	Phe	Ala	Ala	Gly	Phe	Met	Trp	Leu	Asp	
355							360					365				
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Thr	Lys	Val	Leu	Met	Ala	Ser	Val	Gln	Gly	Ser	Lys	Arg	Arg	Lys	Leu	
420							425					430				
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465	470	475	
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480	485	490	495
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